



## SEQUENCE LISTING

&lt;110&gt; Medical Research Council

&lt;120&gt; Obesity Gene

&lt;130&gt; 18396/1140

&lt;140&gt; 09/484,629

&lt;141&gt; 2000-01-18

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&lt;170&gt; PatentIn version 3.0

&lt;210&gt; 1

&lt;211&gt; 924

&lt;212&gt; DNA

&lt;213&gt; Rattus sp.

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (5)..(607)

&lt;400&gt; 1

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1 5 10 15

ccc cca acc ctg ctc ctt ctg ccc gtg cgc ggc cgc aag acc cgc cac 97  
Pro Pro Thr Leu Leu Leu Leu Pro Val Arg Gly Arg Lys Thr Arg His  
20 25 30

gat ccg cct gcc aag tcc aag gtc ggg cgc gtg aaa atg cct cct gca 145  
Asp Pro Pro Ala Lys Ser Lys Val Gly Arg Val Lys Met Pro Pro Ala  
35 40 45

gtg gac cct gcg gaa ttg ttc gtg ttg acc gag cgc tac cga cag tac 193  
Val Asp Pro Ala Glu Leu Phe Val Leu Thr Glu Arg Tyr Arg Gln Tyr  
50 55 60

cgg gag acg gtg cgc gct ctc agg cga gag ttc aca ttg gag gtg cga 241  
Arg Glu Thr Val Arg Ala Leu Arg Arg Glu Phe Thr Leu Glu Val Arg  
65 70 75

ggg aaa ttg cac gag gcc cga gcc ggg gtt ctg gct gag cgc aag gcg 289  
Gly Lys Leu His Glu Ala Arg Ala Gly Val Leu Ala Glu Arg Lys Ala  
80 85 90 95

caa gag gcc atc aga gag cac cag gag ctg atg gcc tgg aac cgg gag 337  
Gln Glu Ala Ile Arg Glu His Gln Glu Leu Met Ala Trp Asn Arg Glu  
100 105 110

gag aac cgg aga ctg cag gaa cta cgg ata gct agg ttg cag ctc gaa 385  
Glu Asn Arg Arg Leu Gln Glu Leu Arg Ile Ala Arg Leu Gln Leu Glu  
115 120 125

gca cag gcc cag gag ctg cgg cag gct gag gtc cag gcc cag agg gcc 433

Ala Gln Ala Gln Glu Leu Arg Gln Ala Glu Val Gln Ala Gln Arg Ala	
130 135 140	
cag gag gag cag gct tgg gtg caa ctg aaa gaa caa gaa gtt ctc aaa	481
Gln Glu Glu Gln Ala Trp Val Gln Leu Lys Glu Gln Glu Val Leu Lys	
145 150 155	
ctg cag gag gag gcc aaa aac ttc atc act cgg gag aac ctg gag gca	529
Leu Gln Glu Glu Ala Lys Asn Phe Ile Thr Arg Glu Asn Leu Glu Ala	
160 165 170 175	
cgg ata gaa gag gcc ttg gac tct ccg aag agt tat aac tgg gcg gtc	577
Arg Ile Glu Glu Ala Leu Asp Ser Pro Lys Ser Tyr Asn Trp Ala Val	
180 185 190	
acc aaa gaa ggg cag gtg gtc agg aac tga gaacagaggc ctctcaggcc	627
Thr Lys Glu Gly Gln Val Val Arg Asn	
195 200	
caaataagga cagtgccttgc ctagggactg gatattgggg tagaaattgg tgcattcccag	687
gaggggtggca cagccttgtc cagagcagcc cccattcatt ctgattttgg caccaggtat	747
agtacctgtt ctgacaccac atacaaactc cggacagcat taaactcttg gaagttccta	807
tcacacagaa gatcagactg gactgtcccc tctagaagcc aagagctgtc tcctgagttt	867
cttggaatag tgtgagccca atgtttcctg cttttataaa taaactattg gaaagca	924

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 <211> 200  
 <212> PRT  
 <213> Rattus sp.

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Pro Thr Leu Leu Leu Leu Pro Val Arg Gly Arg Lys Thr Arg His Asp	
20 25 30	
Pro Pro Ala Lys Ser Lys Val Gly Arg Val Lys Met Pro Pro Ala Val	
35 40 45	
Asp Pro Ala Glu Leu Phe Val Leu Thr Glu Arg Tyr Arg Gln Tyr Arg	
50 55 60	
Glu Thr Val Arg Ala Leu Arg Arg Glu Phe Thr Leu Glu Val Arg Gly	
65 70 75 80	
Lys Leu His Glu Ala Arg Ala Gly Val Leu Ala Glu Arg Lys Ala Gln	
85 90 95	

Glu Ala Ile Arg Glu His Gln Glu Leu Met Ala Trp Asn Arg Glu Glu  
 100 105 110

Asn Arg Arg Leu Gln Glu Leu Arg Ile Ala Arg Leu Gln Leu Glu Ala  
 115 120 125

Gln Ala Gln Glu Leu Arg Gln Ala Glu Val Gln Ala Gln Arg Ala Gln  
 130 135 140

Glu Glu Gln Ala Trp Val Gln Leu Lys Glu Gln Glu Val Leu Lys Leu  
 145 150 155 160

Gln Glu Glu Ala Lys Asn Phe Ile Thr Arg Glu Asn Leu Glu Ala Arg  
 165 170 175

Ile Glu Glu Ala Leu Asp Ser Pro Lys Ser Tyr Asn Trp Ala Val Thr  
 180 185 190

Lys Glu Gly Gln Val Val Arg Asn  
 195 200

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 <211> 998  
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 <213> Rattus sp.

<220>  
 <221> CDS  
 <222> (1)..(996)

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 cgg gcc cct ctg gtg ctg cca gcg cgc ggc cgc aag acc cgc cac gac 96  
 Arg Ala Pro Leu Val Leu Pro Ala Arg Gly Arg Lys Thr Arg His Asp  
 20 25 30  
 ccg ctg gcc aaa tcc aag atc gag cga gtg aac atg ccg ccc gcg gtg 144  
 Pro Leu Ala Lys Ser Lys Ile Glu Arg Val Asn Met Pro Pro Ala Val  
 35 40 45  
 gac cct gcg gag ttc ttc gtg ctg atg gag cgt tac cag cac tac cgc 192  
 Asp Pro Ala Glu Phe Phe Val Leu Met Glu Arg Tyr Gln His Tyr Arg  
 50 55 60  
 cag acc gtg cgc gcc ctg agg atg gag ttc gtg tcc gag gtg cag agg 240  
 Gln Thr Val Arg Ala Leu Arg Met Glu Phe Val Ser Glu Val Gln Arg  
 65 70 75 80  
 aag gtg cac gag gcc cga gcc ggg gtt ctg gcg gag cgc aag gcc ctg 288  
 Lys Val His Glu Ala Arg Ala Gly Val Leu Ala Glu Arg Lys Ala Leu  
 85 90 95

aag gac gcc gcc gag cac cgc gag ctg atg gcc tgg aac cag gcg gag Lys Asp Ala Ala Glu His Arg Glu Leu Met Ala Trp Asn Gln Ala Glu 100 105 110	336
aac cgg cgg ctg cac gag ctg cgg ata gcg agg ctg cgg cag gag gag Asn Arg Arg Leu His Glu Leu Arg Ile Ala Arg Leu Arg Gln Glu Glu 115 120 125	384
cgg gag cag gag cag cgg cag gcg ttg gag cag gcc cgc aag gcc gaa Arg Glu Gln Glu Gln Arg Gln Ala Leu Glu Gln Ala Arg Lys Ala Glu 130 135 140	432
gag gtg cag gcc tgg gcg cag cgc aag gag cgg gaa gtg ctg cag ctg Glu Val Gln Ala Trp Ala Gln Arg Lys Glu Arg Glu Val Leu Gln Leu 145 150 155 160	480
cag gaa gag gtg aaa aac ttc atc acc cga gag aac ctg gag gca cgg Gln Glu Glu Val Lys Asn Phe Ile Thr Arg Glu Asn Leu Glu Ala Arg 165 170 175	528
gtg gaa gca gca ttg gac tcc cgg aag aac tac aac tgg gcc atc acc Val Glu Ala Ala Leu Asp Ser Arg Lys Asn Tyr Asn Trp Ala Ile Thr 180 185 190	576
aga gag ggg ctg gtg gtc agg cca caa cgc agg gac tcc tag ggg ccc Arg Glu Gly Leu Val Val Arg Pro Gln Arg Arg Asp Ser Gly Pro 195 200 205	624
agt aag gac agt gcc cgc cag gga cca tgt atg tat cat ggc gga aga Ser Lys Asp Ser Ala Arg Gln Gly Pro Cys Met Tyr His Gly Gly Arg 210 215 220	672
gtt ggc cct gac ctg gaa taa agc agt tgg tgt tgc tta tga gga agg Val Gly Pro Asp Leu Glu Ser Ser Trp Cys Cys Leu Gly Arg 225 230 235	720
ttc agc ctt atc cag cac agc ctt cac gtt ttg ccc tct gct gtc acc Phe Ser Leu Ile Gln His Ser Leu His Val Leu Pro Ser Ala Val Thr 240 245 250	768
act tgg tca gaa act tcc aaa cgc agt gcc ctg ttc tgc cgg tgt gta Thr Trp Ser Glu Thr Ser Lys Arg Ser Ala Leu Phe Cys Arg Cys Val 255 260 265	816
aag cct cag cgc acc agg aga ccc tag agt ggt ttc cat ctc aca gag Lys Pro Gln Arg Thr Arg Arg Pro Ser Gly Phe His Leu Thr Glu 270 275 280	864
aat cag aca ggc cac agc ccc ctc agg cag cca ggt cat ctg agt atc Asn Gln Thr Gly His Ser Pro Leu Arg Gln Pro Gly His Leu Ser Ile 285 290 295 300	912
att aag agt agt gat ggg aag att aca gtc tga ggg cca aac gtg cct Ile Lys Ser Ser Asp Gly Lys Ile Thr Val Gly Pro Asn Val Pro 305 310 315	960
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20 25 30

Pro Leu Ala Lys Ser Lys Ile Glu Arg Val Asn Met Pro Pro Ala Val  
35 40 45

Asp Pro Ala Glu Phe Phe Val Leu Met Glu Arg Tyr Gln His Tyr Arg  
50 55 60

Gln Thr Val Arg Ala Leu Arg Met Glu Phe Val Ser Glu Val Gln Arg  
65 70 75 80

Lys Val His Glu Ala Arg Ala Gly Val Leu Ala Glu Arg Lys Ala Leu  
85 90 95

Lys Asp Ala Ala Glu His Arg Glu Leu Met Ala Trp Asn Gln Ala Glu  
100 105 110

Asn Arg Arg Leu His Glu Leu Arg Ile Ala Arg Leu Arg Gln Glu Glu  
115 120 125

Arg Glu Gln Glu Gln Arg Gln Ala Leu Glu Gln Ala Arg Lys Ala Glu  
130 135 140

Glu Val Gln Ala Trp Ala Gln Arg Lys Glu Arg Glu Val Leu Gln Leu  
145 150 155 160

Gln Glu Glu Val Lys Asn Phe Ile Thr Arg Glu Asn Leu Glu Ala Arg  
165 170 175

Val Glu Ala Ala Leu Asp Ser Arg Lys Asn Tyr Asn Trp Ala Ile Thr  
180 185 190

Arg Glu Gly Leu Val Val Arg Pro Gln Arg Arg Asp Ser  
195 200 205

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<211> 24  
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<400> 5

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Gly Arg Val Gly Pro Asp Leu Glu  
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<213> Rattus sp.

<400> 6

Ser Ser Trp Cys Cys Leu  
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<210> 7  
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<213> Rattus sp.

<400> 7

Gly Arg Phe Ser Leu Ile Gln His Ser Leu His Val Leu Pro Ser Ala  
1 5 10 15

Val Thr Thr Trp Ser Glu Thr Ser Lys Arg Ser Ala Leu Phe Cys Arg  
20 25 30

Cys Val Lys Pro Gln Arg Thr Arg Arg Pro  
35 40

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<212> PRT  
<213> Rattus sp.

<400> 8

Ser Gly Phe His Leu Thr Glu Asn Gln Thr Gly His Ser Pro Leu Arg  
1 5 10 15

Gln Pro Gly His Leu Ser Ile Ile Lys Ser Ser Asp Gly Lys Ile Thr  
20 25 30

Val

<210> 9  
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 <213> Rattus sp.

<400> 9

Gly Pro Asn Val Pro Ala Ser Cys Phe Cys Lys  
 1 5 10

<210> 10  
 <211> 5  
 <212> PRT  
 <213> Rattus sp.

<400> 10

Ser Phe Val Gly Thr  
 1 5

<210> 11  
 <211> 943  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (1)..(615)

<400> 11  
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 Cys His Val Ala Arg Ser Glu Pro Pro Gly Ala Ala Ala Gly Arg Pro  
 1 5 10 15  
 gcc ccc gac ccc gct gct cct gcc cgt gcg cgg ccg caa gac ccg cca 96  
 Ala Pro Asp Pro Ala Ala Pro Ala Arg Ala Arg Pro Gln Asp Pro Pro  
 20 25 30  
 tga ccc gcc tgc caa atc caa ggt cgg acg ggt gca gac gcc tcc cgc 144  
 Pro Ala Cys Gln Ile Gln Gly Arg Thr Gly Ala Asp Ala Ser Arg  
 35 40 45  
 cgt gga ccc tgc gga att ctt cgt gtt gac cga gcg cta cgg aca gta 192  
 Arg Gly Pro Cys Gly Ile Leu Arg Val Asp Arg Ala Leu Arg Thr Val  
 50 55 60  
 ccg gga gac cgt gcg cgc tct cag gct aga gtt cac gtt gga tgt gcg 240  
 Pro Gly Asp Arg Ala Arg Ser Gln Ala Arg Val His Val Gly Cys Ala  
 65 70 75  
 aag gaa att gca cga ggc ccg agc cgg ggt tct ggc cga gcg caa ggc 288  
 Lys Glu Ile Ala Arg Gly Pro Ser Arg Gly Ser Gly Arg Ala Gln Gly  
 80 85 90 95  
 gca gca ggc cat cac gga gca ccg gga gct gat ggc ctg gaa ccg gga 336  
 Ala Ala Gly His His Gly Ala Pro Gly Ala Asp Gly Leu Glu Pro Gly  
 100 105 110

cga gaa ccg gcg aat gca gga gct acg gat agc gag gtt gca gct gga Arg Glu Pro Ala Asn Ala Gly Ala Thr Asp Ser Glu Val Ala Ala Gly	384
115 120 125	
agc aca ggc cca gga ggt gca gaa ggc tga ggc cca gcg cca gag ggc Ser Thr Gly Pro Gly Gly Ala Glu Gly Gly Pro Ala Pro Glu Gly	432
130 135 140	
tca gga gga gca ggc ttg ggt gca act gaa aga gca aga agt gct caa Ser Gly Gly Ala Gly Leu Gly Ala Thr Glu Arg Ala Arg Ser Ala Gln	480
145 150 155	
gct gca gga gga ggc aaa aaa ctt cat cac tcg gga gaa cct gga ggc Ala Ala Gly Gly Gly Lys Lys Leu His His Ser Gly Glu Pro Gly Gly	528
160 165 170	
acg gat aga aga agc gtt gga ctc tcc gaa gag tta caa ctg ggc cgt Thr Asp Arg Arg Ser Val Gly Leu Ser Glu Glu Leu Gln Leu Gly Arg	576
175 180 185 190	
cac caa aga agg gca ggt ggt cag gaa ctg agc aca gag acttctgggg His Gln Arg Arg Ala Gly Gly Gln Glu Leu Ser Thr Glu	625
195 200	
gccccaaataa gcacagtgtc tgccctagggt ctgtgtactg ggataggaat tgggtacatcc	685
caggaggatg gctcagccgt ttccagagca acctcagtca ctccaggctc ggcaactcacc	745
acctgactgg gaactcccag atgtccctgt tctggcacca cagtcaaact gagggcagca	805
ttaaactctg ggaagttcct atcgcacaga ggatcggaact ggactgtgtc cctctagaag	865
ccaagcttgt cttgtaagtc tcttggaagtc ctgtgagcca aatgtttcct gcttttataa	925
ataaagtatt ggagccca	943

<210> 12  
 <211> 32  
 <212> PRT  
 <213> Homo sapiens

<400> 12

Cys His Val Ala Arg Ser Glu Pro Pro Gly Ala Ala Ala Gly Arg Pro
1 5 10 15

Ala Pro Asp Pro Ala Ala Pro Ala Arg Ala Arg Pro Gln Asp Pro Pro
20 25 30

<210> 13  
 <211> 104  
 <212> PRT  
 <213> Homo sapiens

<400> 13

Pro Ala Cys Gln Ile Gln Gly Arg Thr Gly Ala Asp Ala Ser Arg Arg



1                      5                      10                      15  
 Gly Pro Cys Gly Ile Leu Arg Val Asp Arg Ala Leu Arg Thr Val Pro  
                     20                      25                      30  
 Gly Asp Arg Ala Arg Ser Gln Ala Arg Val His Val Gly Cys Ala Lys  
                     35                      40                      45  
 Glu Ile Ala Arg Gly Pro Ser Arg Gly Ser Gly Arg Ala Gln Gly Ala  
                     50                      55                      60  
 Ala Gly His His Gly Ala Pro Gly Ala Asp Gly Leu Glu Pro Gly Arg  
                     65                      70                      75                      80  
 Glu Pro Ala Asn Ala Gly Ala Thr Asp Ser Glu Val Ala Ala Gly Ser  
                     85                      90                      95  
 Thr Gly Pro Gly Gly Ala Glu Gly  
                     100

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 <212> PRT  
 <213> Homo sapiens

<400> 14

Gly Pro Ala Pro Glu Gly Ser Gly Gly Ala Gly Leu Gly Ala Thr Glu  
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 Arg Ala Arg Ser Ala Gln Ala Ala Gly Gly Gly Lys Lys Leu His His  
                     20                      25                      30  
 Ser Gly Glu Pro Gly Gly Thr Asp Arg Arg Ser Val Gly Leu Ser Glu  
                     35                      40                      45  
 Glu Leu Gln Leu Gly Arg His Gln Arg Arg Ala Gly Gly Gln Glu Leu  
                     50                      55                      60  
 Ser Thr Glu  
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<220>  
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<222> (1)..(615)

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ata tag tga gac ctg tgc aag gaa gga tgg agt gca cgt tcc ctg atg	96
Ile Asp Leu Cys Lys Glu Gly Trp Ser Ala Arg Ser Leu Met	
15 20 25	
ttc aga gca acc ctg tgt cac tcc agg tag gtg aga tga gag gaa gag	144
Phe Arg Ala Thr Leu Cys His Ser Arg Val Arg Glu Glu Glu	
30 35 40	
ggg ggc ctt ggc ctg ggc ctc cta cgg gcc tgg aag ttg gga gaa gga	192
Gly Gly Leu Gly Leu Gly Leu Leu Arg Ala Trp Lys Leu Gly Glu Gly	
45 50 55	
tgt aag cag act ctg ttc tct tct gag aaa tat cag gta ttg cag tca	240
Cys Lys Gln Thr Leu Phe Ser Ser Glu Lys Tyr Gln Val Leu Gln Ser	
60 65 70	
gcc cag gct cct cag acc ctc cta agt gca gat tct ctg cag aat ctg	288
Ala Gln Ala Pro Gln Thr Leu Leu Ser Ala Asp Ser Leu Gln Asn Leu	
75 80 85	
gtg ttg aca aca cta atg agt agg atg aga ctt cag ttc cct agc cct	336
Val Leu Thr Thr Leu Met Ser Arg Met Arg Leu Gln Phe Pro Ser Pro	
90 95 100 105	
cac cgt cag ctt ctg att acc aac aac tct ccc aga gga gag cca tct	384
His Arg Gln Leu Leu Ile Thr Asn Asn Ser Pro Arg Gly Glu Pro Ser	
110 115 120	
acc ttt ggg aca gat gct ctc tgc cct gca ctg cct cct gtt tct ctt	432
Thr Phe Gly Thr Asp Ala Leu Cys Pro Ala Leu Pro Pro Val Ser Leu	
125 130 135	
cat tgt aga gga aga tag tac ttt aaa agc ttc ata aat ggt ctc aag	480
His Cys Arg Gly Arg Tyr Phe Lys Ser Phe Ile Asn Gly Leu Lys	
140 145 150	
gtg gga aga ccc cgg ctc agg tga aag agg aca agc gtc acc tca cac	528
Val Gly Arg Pro Arg Leu Arg Lys Arg Thr Ser Val Thr Ser His	
155 160 165	
agg cca ccc agt aga aaa caa gtg atc act gat act gag aac tct ggc	576
Arg Pro Pro Ser Arg Lys Gln Val Ile Thr Asp Thr Glu Asn Ser Gly	
170 175 180	
aat tgc aga gct gcc caa gac cac aac agg gca gtg caa tgcaaggaaa	625
Asn Cys Arg Ala Ala Gln Asp His Asn Arg Ala Val Gln	
185 190 195	
aggtttgttg ctgattgca aacctaaagt ttaaagtgca tcaggagaac gcttactcaa	685
agaggaagtg taagcctaac ttaagtagct agaagctcag aatttcttg c atcagccctg	745
gaagggtaca caggccaccg gtgggcccaga gaaccacacg ctttggggcg gtgtccaagc	805

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cagcgaactg tggctctcaa ggtgcccctc gaccctccca ctctaccoga gactccaggg	925
acgcgatggg ccagacagca agagctccgc ctacgggggc ggggacagga gattcccgtg	985
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gagaacctgg aggcacggat agaagaggcc ttggactctc cgaagagtta taactgggcg	1885
gtcaccaaag aagggcagggt ggtcaggaac tgagaacaga ggcctctcag gcccaaataa	1945
ggacagtgtc tgcctagggg ctggatattg gggtagaaat tgggtgatcc caggagggtg	2005
gcacagcctt gtccagagca gccccattc attctagatt tggcaccagg tatagtacct	2065
gttctgacac cacatacaaa ctccggacag cattaaactc tgggaagttc ctatcacaca	2125
gaagatcaga ctggactgtc ccctctagaa gccaagagct gtctcctgag tttcttgga	2185
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taaggttatt agccaaaagc cagttcacct aactgagcca ggagttagtt atctgctttg	2365
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cggtcagttg ctgtccttca gtgtgtgtaa gcagtggcca gacagcacc ttgggtgtca	2605
tttcaagact ctctcacctt ggtctgcttt acgtttggtt tgatttggtt tgttctggtt	2665

tttgagacga ggcctttcac tggaacctgg cactcagtat ttagactgcc cagccagcta 2725  
 gcctcagaga atgcatctgc gtatgcttgc ctggcgctgg aattcgggtgc acatggcttt 2785  
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 agagctc 2852

<210> 16  
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<400> 16

Pro Leu Trp Ile  
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<210> 17  
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<400> 17

Tyr Thr Cys Lys  
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 <211> 6  
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<400> 18

Gln Thr Ile Arg Ala Ile  
1 5

<210> 19  
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<400> 19

Asp Leu Cys Lys Glu Gly Trp Ser Ala Arg Ser Leu Met Phe Arg Ala  
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Thr Leu Cys His Ser Arg  
20

<210> 20  
 <211> 104  
 <212> PRT

<213> Homo sapiens

<400> 20

Glu Glu Glu Gly Gly Leu Gly Leu Gly Leu Leu Arg Ala Trp Lys Leu  
1 5 10 15

Gly Glu Gly Cys Lys Gln Thr Leu Phe Ser Ser Glu Lys Tyr Gln Val  
20 25 30

Leu Gln Ser Ala Gln Ala Pro Gln Thr Leu Leu Ser Ala Asp Ser Leu  
35 40 45

Gln Asn Leu Val Leu Thr Thr Leu Met Ser Arg Met Arg Leu Gln Phe  
50 55 60

Pro Ser Pro His Arg Gln Leu Leu Ile Thr Asn Asn Ser Pro Arg Gly  
65 70 75 80

Glu Pro Ser Thr Phe Gly Thr Asp Ala Leu Cys Pro Ala Leu Pro Pro  
85 90 95

Val Ser Leu His Cys Arg Gly Arg  
100

<210> 21

<211> 17

<212> PRT

<213> Homo sapiens

<400> 21

Tyr Phe Lys Ser Phe Ile Asn Gly Leu Lys Val Gly Arg Pro Arg Leu  
1 5 10 15

Arg

<210> 22

<211> 37

<212> PRT

<213> Homo sapiens

<400> 22

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